

GAP ALIGNMENT:
SEQ ID NO:3 to Spezyme Ethyl (New Matrix)

GAP of: NewB.pep check: 1170 from: 1 to: 514

WPDEF Seq ID Nos 3, translated by ThreeToOne
none

to: SPEZE.pgp check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: [blosum62.cmp](#) CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	2635	Length:	514
Ratio:	5.444	Gaps:	1
Percent Similarity:	98.967	Percent Identity:	98.967

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Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 2
      . = 1
```

NewB.pep x SPEZE.pep June 3, 2005 11:04 ..

```

1  AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPAYKGT 50
  |||
1  AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPAYKGT 50
  .
51  SRSDVGYGVDLYDLGEFNQKGAVRTKYGTAKAYLQAIQAAHAAGMQVYA 100
  |||
51  SRSDVGYGVDLYDLGEFNQKGTVRTKYGTAKAYLQAIQAAHAAGMQVYA 100
  .
101 DVVFDHKGGADGTEWVD AVEVNPSDRNQEISGTYQIQAWTKFDFFPGRGNT 150
  |||
101 DVVFDHKGGADGTEWVD AVEVNPSDRNQEISGTYQIQAWTKFDFFPGRGNT 150
  .
151 YSSFKWRWYHFDGVDWDESRLKSRIYKFRGIGKAWDWEVDTENGNYDYLM 200
  |||
151 YSSFKWRWYHFDGVDWDESRLKSRIYKF..IGKAWDWEVDTENGNYDYLM 198
  .
201 YADLDMDHPEVVTELKSWGKQYVNTTNIDGFRLDAVKHIKFSFFPDWLSD 250
  |||
199 YADLDMDHPEVVTELKNWGKQYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
  .
251 VRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASK 300

```

GAP Alignment:
 SEQ ID NO:3 to Spezyme Ethyl
 (New Matrix)

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|||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
|||||
301 SGGTFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 350
||| |||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
|||||
351 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 400
|||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
|||||
401 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 450
|||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
|||||
451 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTTVSTIAWSITTRPWT 500
|||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT..... 484

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EXHIBIT 9

GAP ALIGNMENT:
Sequence 3 (Figure 1) to Spezyme Ethyl (Old Matrix)

GAP of: NewA.pep check: 754 from: 1 to: 514

WPDEF A. Figure 1, sequence 3

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: oldpep.cmp CompCheck: 2543
Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National Biomedical Research Foundation, Washington D.C.) rescaled by dividing each value by the sum of its row and column, and normalizing to a mean of 0 and standard deviation of 1.0. The value for FY (Phe-Tyr) = RW = 1.425. Perfect matches are set to 1.5 and no matches on any row are . . .

Gap Weight:	30	Average Match:	5.402
Length Weight:	3	Average Mismatch:	-3.964
Quality:	7203	Length:	514
Ratio:	14.882	Gaps:	1
Percent Similarity:	99.793	Percent Identity:	99.587

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Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 4
      . = 1
```

NewA.pap x SPEZE.pap June 3, 2005 11:06 ..

```

1 aapfngtmmqyfewylpddgtlwtkvaneannlsslgitalwlpPAYKGT 50
  |||
1 AAPFN GTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50

51 srsdvgygvydlydlgefngkgktvrtykgtkaqylqaiqaahaagmqvya 100
  |||
51 SRSDVG YGYVDLYDLGEFNQKGKTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100

101 dvvfdhkgggadgtewvdavevnpsdrnqeisgtyqiqawtkfdpgrgnt 150
  |||
101 DVVFDH KGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDPFGRGNT 150

151 yssfkwrrwyhfdgvdwdesrklrsriykfrgigkawdwewdtengnydylm 200
  |||
151 YSSFKWRWYHFDGVDWDESRLRSRIYKF..IGKAWDWEVDTENGNYDYL M 198

201 yadldmdhpevvvtelknwkgkwyvnttnidgfrldavkhikfsffpdwlsy 250
  |||
199 YADLDMDHPEVVVTE LKNWKGK WYVNTT NIDGFR LD AVKH I KFSFFPDWLSY 248

```

GAP Alignment:
Sequence 3 (Figure 1) to Spezyme Ethyl
(Old Matrix)

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251 vrsqtgkplftvgeywsydinklhnyitktgdgtmslfdaplnkfytask 300
    |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298

301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepggalqswvdpwfkpla 350
    |||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348

351 yafiltrqegypcvfygdyygipqynipslkskidplliarrrdyaygtqh 400
    |||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398

401 dyldhsdiigwtreggtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
    |||||||||||||.|||||||||||||||||||||
399 DYLDHSDIIGWTRREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448

451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvstiarppittrpwt 500
    |||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSSVSVWVPRKTT..... 484

```

EXHIBIT 10

GAP ALIGNMENT:
Sequence 3 (Figure 1) to Spezyme Ethyl (New Matrix)

GAP of: NewA.pap check: 754 from: 1 to: 514

WPDEF A. Figure 1, sequence 3

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: [blosum62.cmp](#) CompCheck: 1102
 BLOSUM62 amino acid substitution matrix.
 Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

```

Quality:      2653      Length:      514
Ratio:       5.481      Gaps:        1
Percent Similarity: 99.587  Percent Identity: 99.587

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```
Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 2
      . = 1
```

NewA.ppt x SPEZE.ppt June 3, 2005 11:03 ..

[illegible]

GAP Alignment:
Sequence 3 (Figure 1) to Spezyme Ethyl
(New Matrix)

```

249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepggalqswvdpwfkpla 350
    ||||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
    ||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
401 dyldhsdiigwtreggtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
    ||||||||||||||||||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTRREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVfy 448
451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvstiarppitttrpwt 500
    ||||||||||||||||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGsvsvwvprktt..... 484

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EXHIBIT 11

Alpha-Amylase Alignments

Spezyme	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50
SEQ ID NO:3	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50
Figure 1	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50
ATCC 31,195	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50

Spezyme	SRSDVGYG	DLYDLGEFNQ	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100
SEQ ID NO:3	SRSDVGYG	DLYDLGEFNQ	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100
Figure 1	SRSDVGYG	DLYDLGEFNQ	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100
ATCC 31,195	SRSDVGYG	DLYDLGEFNQ	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100

Spezyme	DVVFDPKGG	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFPGRGNT	150
SEQ ID NO:3	DVVFDPKGG	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFPGRGNT	150
Figure 1	DVVFDPKGG	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFPGRGNT	150
ATCC 31,195	DVVFDPKGG	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFPGRGNT	150

Spezyme	YSSFQKRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	198
SEQ ID NO:3	YSSFQKRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	200
Figure 1	YSSFQKRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	200
ATCC 31,195	YSSFQKRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	200

Spezyme	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	248
SEQ ID NO:3	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	250
Figure 1	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	250
ATCC 31,195	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	250

Spezyme	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	298
SEQ ID NO:3	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	300
Figure 1	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	300
ATCC 31,195	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	300

Alpha-Amylase Alignments

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Spezyme	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	348
SEQ ID NO:3	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	350
Figure 1	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	350
ATCC 31,195	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	350

Spezyme	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	398
SEQ ID NO:3	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	400
Figure 1	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	400
ATCC 31,195	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	400

Spezyme	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	448
SEQ ID NO:3	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	450
Figure 1	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	450
ATCC 31,195	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	450

Spezyme	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTT		484
SEQ ID NO:3	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTTVSTI	AWSITTRPWT	500
Figure 1	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTTVSTI	ARPITTRPWT	500
ATCC 31,195	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTTVST		489

Spezyme						
SEQ ID NO:3	DEFVRWTEPR	LVAW				514
Figure 1	GEFVRWTEPR	LVAW				514
ATCC 31,195						